

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:38:39 ; Search time 35297.7 Seconds  
(without alignments)  
17607.528 Million cell updates/sec

Title: US-10-757-343-2  
Perfect score: 9719  
Sequence: 1 tggaagggctaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
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2: gb\_pat:\*  
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8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	9531.2	98.1	9719	2	AR268768	AR268768 Sequence	
2	9531.2	98.1	9719	10	HIVHXB2CG	K03455 Human immun	

3	9513.6	97.9	9770	10	HIVPV22	K02083 Human immun
4	9511.6	97.9	9749	2	I07983	I07983 Sequence 1
5	9507	97.8	9748	10	REHTLV3	X01762 Human T-cel
6	9499	97.7	9748	2	E01099	E01099 DNA sequenc
7	9487	97.6	9752	10	HIVMCK1	D86068 Human immun
8	9478.6	97.5	9754	10	HIV2132	D86069 Human immun
9	9433.8	97.1	9609	2	AR607371	AR607371 Sequence
10	9433.8	97.1	9609	10	HIV1U12055	U12055 Human immun
11	9385.6	96.6	9795	10	HIVTH475A	L31963 Human immun
12	9208.4	94.7	14824	8	AF324493	AF324493 HIV-1 vec
13	9206.8	94.7	9709	2	AR067813	AR067813 Sequence
14	9206.8	94.7	9709	2	BD238372	BD238372 Virus vac
15	9206.8	94.7	9709	2	AR224437	AR224437 Sequence
16	9206.8	94.7	9709	2	AR352469	AR352469 Sequence
17	9206.8	94.7	9709	2	AX032749	AX032749 Sequence
18	9206.8	94.7	9709	10	HIVNL43	M19921 Human immun
19	9109	93.7	9781	10	HIVF12CG	Z11530 Human Immun
20	9084	93.5	9699	10	AF070521	AF070521 HIV-1 E9
21	9001.2	92.6	9181	2	AX074066	AX074066 Sequence
22	9001.2	92.6	9181	10	AF033819	AF033819 HIV-1, co
23	8979.8	92.4	9193	2	A04321	A04321 Human immun
24	8975.4	92.3	9213	2	E00987	E00987 Genomic DNA
25	8970.6	92.3	9193	2	A07867	A07867 Human immun
26	8952.4	92.1	9213	2	I04549	I04549 Sequence 11
27	8940.8	92.0	9229	10	HIVBRUCG	K02013 Human immun
28	8928.2	91.9	9688	10	AY835754	AY835754 HIV-1 iso
29	8903.6	91.6	9697	10	AY835779	AY835779 HIV-1 iso
30	8900	91.6	9730	10	AY835770	AY835770 HIV-1 iso
31	8859	91.2	9688	10	AY835765	AY835765 HIV-1 iso
32	8836.8	90.9	9733	10	AY835771	AY835771 HIV-1 iso
33	8826.2	90.8	9703	10	AY835762	AY835762 HIV-1 iso
34	8823.6	90.8	9712	10	AY835781	AY835781 HIV-1 iso
35	8819.8	90.7	9703	10	AY835777	AY835777 HIV-1 iso
36	8814.8	90.7	9747	10	AY835759	AY835759 HIV-1 iso
37	8806.8	90.6	9715	10	AY835766	AY835766 HIV-1 iso
38	8793	90.5	9718	10	AY835749	AY835749 HIV-1 iso
39	8791.2	90.5	9700	10	AY835755	AY835755 HIV-1 iso
40	8788.4	90.4	9715	10	AF004394	AF004394 HIV-1 str
41	8782.8	90.4	9749	10	AY835760	AY835760 HIV-1 iso
42	8780.8	90.3	9739	10	AF042101	AF042101 HIV-1 iso
43	8774	90.3	9711	10	HIVYU10X	M93259 Human immun
44	8767.2	90.2	9739	10	AF003887	AF003887 HIV-1 chi
45	8763.8	90.2	9664	10	AY835780	AY835780 HIV-1 iso

#### ALIGNMENTS

##### RESULT 1

AR268768

LOCUS AR268768 9719 bp DNA linear PAT 10-APR-2003  
 DEFINITION Sequence 1 from patent US 6500623.  
 ACCESSION AR268768  
 VERSION AR268768.1 GI:29699384  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 15:50:12 ; Search time 347.96 Seconds  
 (without alignments)  
 16207.366 Million cell updates/sec

Title: US-10-757-343-3  
 Perfect score: 3014  
 Sequence: 1 ggcgggccgctctagactag.....ggatccgcggccgctctaga 3014

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
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 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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c 1	2759	91.5	5108	3	US-09-628-730-51		Sequence 51, Appl
c 2	2759	91.5	5108	3	US-09-628-730-52		Sequence 52, Appl
c 3	2759	91.5	5111	3	US-09-628-730-55		Sequence 55, Appl
c 4	2759	91.5	5185	3	US-09-628-730-47		Sequence 47, Appl
c 5	2759	91.5	5188	3	US-09-628-730-59		Sequence 59, Appl
c 6	2759	91.5	5254	3	US-09-628-730-60		Sequence 60, Appl
c 7	2754.2	91.4	5899	3	US-09-173-053-2		Sequence 2, Appli

c	8	2742.2	91.0	5845	3	US-09-173-053-1	Sequence 1, Appli
c	9	2665.2	88.4	6978	3	US-09-872-733A-15	Sequence 15, Appl
c	10	2665.2	88.4	8366	3	US-09-872-733A-6	Sequence 6, Appli
c	11	2662.2	88.3	5900	2	US-08-663-998-1	Sequence 1, Appli
c	12	2662.2	88.3	5952	2	US-08-663-998-2	Sequence 2, Appli
c	13	2660.6	88.3	5676	2	US-08-663-998-3	Sequence 3, Appli
c	14	2660.6	88.3	5682	2	US-08-663-998-4	Sequence 4, Appli
c	15	2427.6	80.5	15538	3	US-09-554-337-1	Sequence 1, Appli
c	16	2418.2	80.2	4864	3	US-09-340-798A-1	Sequence 1, Appli
c	17	2418.2	80.2	4864	4	US-09-393-803-14	Sequence 14, Appl
c	18	2418.2	80.2	7003	3	US-09-913-909-1	Sequence 1, Appli
c	19	2418.2	80.2	7073	3	US-09-913-909-2	Sequence 2, Appli
c	20	2418.2	80.2	7272	3	US-09-913-909-4	Sequence 4, Appli
c	21	2418.2	80.2	7285	3	US-09-913-909-3	Sequence 3, Appli
c	22	2416.6	80.2	4865	5	US-10-204-200-1	Sequence 1, Appli
c	23	2394.6	79.4	4915	3	US-09-173-053-7	Sequence 7, Appli
c	24	2149.4	71.3	5859	5	US-09-826-206A-3	Sequence 3, Appli
	25	1898.4	63.0	4646	3	US-09-485-286-14	Sequence 14, Appl
	26	1805.4	59.9	4296	2	US-08-316-950-15	Sequence 15, Appl
	27	1805.4	59.9	4296	7	PCT-US95-12642-15	Sequence 15, Appl
	28	1805.4	59.9	4352	2	US-08-316-950-16	Sequence 16, Appl
	29	1805.4	59.9	4352	7	PCT-US95-12642-16	Sequence 16, Appl
	30	1805.4	59.9	6047	2	US-08-316-950-12	Sequence 12, Appl
	31	1805.4	59.9	6047	7	PCT-US95-12642-12	Sequence 12, Appl
	32	1769.4	58.7	3993	2	US-08-316-950-14	Sequence 14, Appl
	33	1769.4	58.7	3993	7	PCT-US95-12642-14	Sequence 14, Appl
	34	1769.4	58.7	6044	2	US-08-316-950-18	Sequence 18, Appl
	35	1769.4	58.7	6044	7	PCT-US95-12642-18	Sequence 18, Appl
	36	1768.4	58.7	4120	2	US-07-977-630-20	Sequence 20, Appl
c	37	1768.4	58.7	4120	2	US-07-977-630-21	Sequence 21, Appl
	38	1768.4	58.7	4120	2	US-08-316-950-11	Sequence 11, Appl
	39	1768.4	58.7	4120	7	PCT-US95-12642-11	Sequence 11, Appl
	40	1768.4	58.7	4505	2	US-08-316-950-13	Sequence 13, Appl
	41	1768.4	58.7	4505	7	PCT-US95-12642-13	Sequence 13, Appl
	42	1768.4	58.7	6171	2	US-08-316-950-17	Sequence 17, Appl
	43	1768.4	58.7	6171	7	PCT-US95-12642-17	Sequence 17, Appl
c	44	1499.6	49.8	3987	3	US-09-082-649B-83	Sequence 83, Appl
c	45	1499.6	49.8	3987	3	US-09-965-101-83	Sequence 83, Appl

# ALIGNMENTS

## RESULT 1

US-09-628-730-51/c

; Sequence 51, Application US/09628730

; Patent No. 6759393

; GENERAL INFORMATION:

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE

; TITLE OF INVENTION: COMPOSITIONS

; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730

; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 51

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 02:58:50 ; Search time 27527.4 Seconds  
 (without alignments)  
 19743.258 Million cell updates/sec

Title: US-10-757-343-2  
 Perfect score: 9719  
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Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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c	1	466	4.8	527	11	BH886550	BH886550 LB00861a.
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	3	416.8	4.3	462	5	CK084149	CK084149 77655rsic

	4	416.8	4.3	462	8	CO838386	CO838386 LM_GL5_00
	5	416.8	4.3	467	5	CK084626	CK084626 84293rsic
	6	414.8	4.3	443	5	CK084791	CK084791 84281rsic
	7	411.8	4.2	443	5	CK084400	CK084400 83872rsic
	8	411.8	4.2	448	5	CK077577	CK077577 79154rsic
c	9	411.2	4.2	839	14	DU665892	DU665892 Ciuffi-HI
	10	410.6	4.2	843	14	DU667159	DU667159 Ciuffi-HI
	11	410.6	4.2	852	14	DU665880	DU665880 Ciuffi-HI
	12	404.8	4.2	459	5	CK080759	CK080759 79881rsic
c	13	404.4	4.2	845	14	DU667190	DU667190 Ciuffi-HI
	14	399.8	4.1	445	5	CK083896	CK083896 85763rsic
	15	399.8	4.1	448	5	CK081454	CK081454 81192rsic
c	16	397.4	4.1	818	14	DU666770	DU666770 Ciuffi-HI
	17	395.8	4.1	432	5	CK078909	CK078909 84577rsic
	18	392.2	4.0	422	8	CO838387	CO838387 LM_GL5_00
	19	391.8	4.0	432	5	CK076236	CK076236 77446rsic
	20	390.8	4.0	419	5	CK076309	CK076309 79822rsic
	21	390.8	4.0	431	8	CV101630	CV101630 UMC-pcryb
	22	384.8	4.0	425	5	CK077626	CK077626 85348rsic
	23	382.8	3.9	423	5	CK081960	CK081960 84291rsic
c	24	356.2	3.7	364	14	DU638111	DU638111 Ciuffi-HI
c	25	301.2	3.1	342	8	CV101352	CV101352 UMC-pcryb
	26	297.8	3.1	348	5	CK080432	CK080432 84150rsic
c	27	297.2	3.1	317	1	AB036462	AB036462 AB036462
c	28	282.6	2.9	330	13	CL293849	CL293849 02S0349-0
	29	251.6	2.6	284	5	CK078901	CK078901 77490rsic
	30	171.2	1.8	199	5	CK084529	CK084529 86382rsic
c	31	169.2	1.7	592	14	DU637731	DU637731 Ciuffi-HI
c	32	163.2	1.7	835	14	DU666050	DU666050 Ciuffi-HI
	33	163.2	1.7	849	14	DU667286	DU667286 Ciuffi-HI
	34	145.8	1.5	1339	14	DU799820	DU799820 lv01_fp00
	35	139.4	1.4	1381	14	DU799984	DU799984 lv01_fp00
	36	138.8	1.4	1347	14	DU799995	DU799995 lv01_fp00
	37	137.6	1.4	1396	14	DU799626	DU799626 lv01_fp00
	38	137.4	1.4	1414	14	DU799673	DU799673 lv01_fp00
	39	137	1.4	1360	14	DU800625	DU800625 lv01_fp00
	40	136.4	1.4	1385	14	DU799681	DU799681 lv01_fp00
	41	136.2	1.4	1368	14	DU799697	DU799697 lv01_fp00
	42	135.6	1.4	1217	14	DU800092	DU800092 lv01_fp00
	43	135.6	1.4	1383	14	DU799713	DU799713 lv01_fp00
	44	135.2	1.4	1380	14	DU799993	DU799993 lv01_fp00
	45	135	1.4	1370	14	DU799677	DU799677 lv01_fp00

# ALIGNMENTS

## RESULT 1

BH886550/c

LOCUS BH886550 527 bp DNA linear GSS 07-AUG-2002

DEFINITION LB00861a.d\_SP6.1 Leishmania major Friedlin BAC Library Leishmania major genomic clone LB00861a, genomic survey sequence.

ACCESSION BH886550

VERSION BH886550.1 GI:22130945

KEYWORDS GSS.

SOURCE Leishmania major

ORGANISM Leishmania major

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:38:39 ; Search time 10946.3 Seconds  
 (without alignments)  
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Title: US-10-757-343-3  
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 Maximum Match 100%  
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Database : GenEmbl:\*  
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 2: gb\_pat:\*  
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 4: gb\_pl:\*  
 5: gb\_pr:\*  
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 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

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# SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
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c	2	2759	91.5	5108	2	BD000698	BD000698 Growth ho



c	3	2759	91.5	5108	2	AR562804	AR562804	Sequence
c	4	2759	91.5	5108	2	AR562805	AR562805	Sequence
c	5	2759	91.5	5108	2	AX138932	AX138932	Sequence
c	6	2759	91.5	5108	2	AX138933	AX138933	Sequence
c	7	2759	91.5	5111	2	BD000701	BD000701	Growth ho
c	8	2759	91.5	5111	2	AR562808	AR562808	Sequence
c	9	2759	91.5	5111	2	AX138936	AX138936	Sequence
c	10	2759	91.5	5185	2	BD000693	BD000693	Growth ho
c	11	2759	91.5	5185	2	AR562800	AR562800	Sequence
c	12	2759	91.5	5185	2	AX138928	AX138928	Sequence
c	13	2759	91.5	5188	2	BD000705	BD000705	Growth ho
c	14	2759	91.5	5188	2	AR562812	AR562812	Sequence
c	15	2759	91.5	5188	2	AX138940	AX138940	Sequence
c	16	2759	91.5	5254	2	BD000706	BD000706	Growth ho
c	17	2759	91.5	5254	2	AR562813	AR562813	Sequence
c	18	2759	91.5	5254	2	AX138941	AX138941	Sequence
c	19	2754.2	91.4	5899	2	AR231272	AR231272	Sequence
c	20	2754.2	91.4	7528	2	AX080953	AX080953	Sequence
c	21	2746.2	91.1	7521	2	AX080951	AX080951	Sequence
c	22	2742.2	91.0	5845	2	AR231271	AR231271	Sequence
c	23	2692.6	89.3	11358	2	BD008820	BD008820	Compositi
c	24	2665.2	88.4	6978	2	AR435506	AR435506	Sequence
c	25	2665.2	88.4	7099	2	AX180761	AX180761	Sequence
c	26	2665.2	88.4	8366	2	AR435498	AR435498	Sequence
c	27	2665.2	88.4	8366	2	AX180752	AX180752	Sequence
c	28	2662.2	88.3	4779	2	AX080955	AX080955	Sequence
c	29	2662.2	88.3	5310	2	AX080989	AX080989	Sequence
c	30	2662.2	88.3	5322	2	AX080956	AX080956	Sequence
c	31	2662.2	88.3	5900	2	AR064320	AR064320	Sequence
c	32	2662.2	88.3	5900	2	BD008816	BD008816	Compositi
c	33	2662.2	88.3	5952	2	AR064321	AR064321	Sequence
c	34	2662.2	88.3	5952	2	BD008817	BD008817	Compositi
c	35	2660.6	88.3	5676	2	AR064322	AR064322	Sequence
c	36	2660.6	88.3	5676	2	BD008818	BD008818	Compositi
c	37	2660.6	88.3	5682	2	AR064323	AR064323	Sequence
c	38	2660.6	88.3	5682	2	BD008819	BD008819	Compositi
c	39	2437.8	80.9	6319	2	CS078974	CS078974	Sequence
c	40	2436.2	80.8	5039	2	CS078949	CS078949	Sequence
c	41	2436.2	80.8	5549	2	AX427842	AX427842	Sequence
c	42	2436.2	80.8	5549	2	AX427843	AX427843	Sequence
c	43	2436.2	80.8	5549	2	AX427844	AX427844	Sequence
c	44	2436.2	80.8	5549	2	AX427845	AX427845	Sequence
c	45	2436.2	80.8	6096	2	CS078963	CS078963	Sequence

#### ALIGNMENTS

##### RESULT 1

BD000697/c

LOCUS BD000697 5108 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Growth hormone and growth hormone-releasing hormone composition.  
 ACCESSION BD000697  
 VERSION BD000697.1 GI:18623810  
 KEYWORDS JP 2000350590-A/50.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct



OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 15:50:12 ; Search time 1122.04 Seconds  
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 16207.366 Million cell updates/sec

Title: US-10-757-343-2  
 Perfect score: 9719  
 Sequence: 1 tggaagggctaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	9531.2	98.1	9719	3	US-09-700-304-1	Sequence 1, Appli
2	9433.8	97.1	9609	3	US-09-827-688-4	Sequence 4, Appli
3	9206.8	94.7	9709	2	US-08-188-583-5	Sequence 5, Appli
4	9206.8	94.7	9709	3	US-08-388-353-1	Sequence 1, Appli
5	9206.8	94.7	9709	3	US-08-488-551B-1	Sequence 1, Appli
6	9206.8	94.7	9709	3	US-09-309-572-15	Sequence 15, Appl
7	9206.8	94.7	9709	3	US-09-718-096-15	Sequence 15, Appl

8	8724	89.8	8933	3	US-08-463-210-4	Sequence 4, Appli
9	8724	89.8	8933	3	US-09-620-958A-3	Sequence 3, Appli
10	8724	89.8	8933	3	US-08-463-028-4	Sequence 4, Appli
11	8724	89.8	8933	3	US-08-463-209-4	Sequence 4, Appli
12	8724	89.8	8933	3	US-09-943-286-3	Sequence 3, Appli
13	8723	89.8	8932	3	US-09-124-900-1	Sequence 1, Appli
14	8711.2	89.6	8933	3	US-09-620-958A-4	Sequence 4, Appli
15	8711.2	89.6	8933	3	US-09-943-286-4	Sequence 4, Appli
16	8706.4	89.6	8933	3	US-09-620-958A-9	Sequence 9, Appli
17	8706.4	89.6	8933	3	US-09-943-286-9	Sequence 9, Appli
18	8668	89.2	9746	2	US-08-022-835-3	Sequence 3, Appli
19	8668	89.2	9746	2	US-08-388-809-3	Sequence 3, Appli
20	8668	89.2	9746	2	US-08-647-714-3	Sequence 3, Appli
21	8666.4	89.2	9739	2	US-08-022-835-1	Sequence 1, Appli
22	8666.4	89.2	9739	2	US-08-388-809-1	Sequence 1, Appli
23	8666.4	89.2	9739	2	US-08-647-714-1	Sequence 1, Appli
24	8582.8	88.3	9737	2	US-08-944-449-7	Sequence 7, Appli
25	8582.8	88.3	9737	3	US-09-353-362-7	Sequence 7, Appli
26	8582.8	88.3	9737	3	US-09-827-688-12	Sequence 12, Appl
27	8484.4	87.3	15581	3	US-08-646-538-35	Sequence 35, Appl
28	8484.4	87.3	15581	3	US-09-503-222-35	Sequence 35, Appl
29	7616.4	78.4	12494	3	US-08-935-312-13	Sequence 13, Appl
30	7616.4	78.4	12494	3	US-08-848-760B-33	Sequence 33, Appl
31	7611.4	78.3	12479	3	US-09-318-138-13	Sequence 13, Appl
32	7351.4	75.6	9207	3	US-08-388-353-800	Sequence 800, App
33	7351.4	75.6	9207	3	US-08-488-551B-800	Sequence 800, App
34	7299.2	75.1	8954	3	US-09-184-418C-6	Sequence 6, Appli
35	7299.2	75.1	8954	3	US-10-290-579A-6	Sequence 6, Appli
36	7055.6	72.6	9913	3	US-09-827-688-11	Sequence 11, Appl
37	6772.4	69.7	8953	3	US-09-184-418C-3	Sequence 3, Appli
38	6772.4	69.7	8953	3	US-10-290-579A-3	Sequence 3, Appli
39	6719.2	69.1	8992	3	US-09-184-418C-4	Sequence 4, Appli
40	6719.2	69.1	8992	3	US-10-290-579A-4	Sequence 4, Appli
41	6713.8	69.1	8968	3	US-09-184-418C-1	Sequence 1, Appli
42	6713.8	69.1	8968	3	US-10-290-579A-1	Sequence 1, Appli
43	6600	67.9	8972	3	US-09-184-418C-9	Sequence 9, Appli
44	6600	67.9	8972	3	US-10-290-579A-9	Sequence 9, Appli
45	6584.8	67.8	9010	3	US-09-184-418C-8	Sequence 8, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-700-304-1

```

; Sequence 1, Application US/09700304
; Patent No. 6500623
; GENERAL INFORMATION:
; APPLICANT: GeneCure, LLC
; APPLICANT: Tung, Frank Y.T.
; TITLE OF INVENTION: Replication Defective HIV Vaccine
; FILE REFERENCE: 00714PCTUS
; CURRENT APPLICATION NUMBER: US/09/700,304
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: PCT/US99/10523
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/085,115

```

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:23:04 ; Search time 3629.45 Seconds  
(without alignments)  
18670.376 Million cell updates/sec

Title: US-10-757-343-2  
Perfect score: 9719  
Sequence: 1 tggaagggctaattcactcc.....gtggaaaatctctagcaggt 9719

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
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4: geneseqn2001as:\*  
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6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	9719	100.0	9719	13	ADQ91504	Adq91504 DNA const	
2	9531.2	98.1	9719	11	ADM73881	Adm73881 HIV-1 str	

3	9531.2	98.1	9719	12	ADO52557	Ado52557 Human imm
4	9531.2	98.1	9719	14	AEB54637	Aeb54637 HIV-1 (HX
5	9531.2	98.1	9719	14	AED64721	Aed64721 Human imm
6	9518	97.9	9749	2	AAQ45922	Aaq45922 HTLV-III
7	9442.6	97.2	9745	1	AAN60240	Aan60240 HTLV-III
8	9433.8	97.1	9609	6	AAD25515	Aad25515 Human imm
9	9259.6	95.3	9965	6	ABQ81389	Abq81389 HIV-1 R8
10	9210	94.8	9709	12	ADP84804	Adp84804 HIV-1 hyb
11	9208.4	94.7	14824	15	AEE40105	Aee40105 HIV1 NL4-
12	9206.8	94.7	9709	2	AAQ96140	Aaq96140 HIV-1 NL4
13	9206.8	94.7	9709	2	AAV81871	Aav81871 Nucleic a
14	9206.8	94.7	9709	3	AAA40298	Aaa40298 HIV-1 vir
15	9206.8	94.7	9709	3	AAZ88127	Aaz88127 HIV-1 NY5
16	9206.8	94.7	9709	3	AAA97926	Aaa97926 HIV-1 env
17	9206.8	94.7	9709	6	ABQ76897	Abq76897 HIV-1 NL4
18	9206.8	94.7	9709	8	ABS57823	Abs57823 HIV-1 gen
19	9206.8	94.7	9709	12	ADO52559	Ado52559 Human imm
20	9206.8	94.7	9709	14	ADZ26365	Adz26365 HIV-1 com
21	9206.8	94.7	9709	14	ADZ26364	Adz26364 HIV-1 pre
22	9206.8	94.7	9709	15	AEF69293	Aef69293 Human imm
23	9205.2	94.7	9709	14	ADZ26366	Adz26366 HIV-1 com
24	9191	94.6	9709	2	AAQ22488	Aaq22488 HIV-1 pro
25	9014.6	92.8	9425	2	AAQ45919	Aaq45919 HTLV-III
26	9001.2	92.6	9181	5	AAF24377	Aaf24377 Human imm
27	9001.2	92.6	9181	8	AAL53720	Aal53720 HIV-1 DNA
28	9001.2	92.6	9181	8	AAD49652	Aad49652 Human imm
29	9001.2	92.6	9181	12	ADN36409	Adn36409 HIV gene
30	8991	92.5	9213	2	AAV74271	Aav74271 HTLV-III
31	8979.8	92.4	9193	10	ACC70123	Acc70123 Nucleotid
32	8975.4	92.3	9213	2	AAV81866	Aav81866 Nucleic a
33	8975.4	92.3	9213	9	ACD27911	Acd27911 Human lym
34	8975.4	92.3	9213	12	ADO26430	Ado26430 Human T-c
35	8966	92.3	9193	6	AAL49920	Aal49920 Lymphaden
36	8964.2	92.2	9213	1	AAN60288	Aan60288 Sequence
37	8960.6	92.2	9427	2	AAQ45920	Aaq45920 HTLV-III
38	8959.6	92.2	9193	1	AAN60365	Aan60365 Sequence
39	8947.4	92.1	9425	2	AAQ45921	Aaq45921 HTLV-III
40	8940.8	92.0	9229	12	ADO52558	Ado52558 Human imm
41	8940.8	92.0	9229	15	AEE70696	Aee70696 CEM15 rec
42	8878.4	91.4	9103	9	ADA49386	Ada49386 Lymphaden
43	8878.4	91.4	9103	12	ADP81476	Adp81476 Lymphaden
44	8878.4	91.4	9103	14	ADZ71144	Adz71144 HIV-1 com
45	8824.2	90.8	9098	9	ADA49378	Ada49378 Lymphaden

# ALIGNMENTS

## RESULT 1

ADQ91504

ID ADQ91504 standard; DNA; 9719 BP.

XX

AC ADQ91504;

XX

DT 21-OCT-2004 (first entry)

XX

DE DNA construct LW, useful for HIV infection prevention, treatment.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 01:23:04 ; Search time 1125.55 Seconds  
 (without alignments)  
 18670.376 Million cell updates/sec

Title: US-10-757-343-3  
 Perfect score: 3014  
 Sequence: 1 ggcgggccgctctagactag.....ggatccgcggccgctctaga 3014

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
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 11: geneseqn2003ds:\*  
 12: geneseqn2004as:\*  
 13: geneseqn2004bs:\*  
 14: geneseqn2005s:\*  
 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			Query				Description
	No.	Score	Match	Length	DB	ID	
c	1	3014	100.0	3014	13	ADQ91505	Adq91505 Plasmid D
	2	2841.6	94.3	3982	6	ABA91505	Aba91505 Vector pl

c	3	2841.6	94.3	3982	12	ADL71104	Adl71104 pGVL1-EGF
c	4	2837.6	94.1	7002	14	ADZ64591	Adz64591 Expressio
c	5	2837.6	94.1	7802	14	ADZ64590	Adz64590 Expressio
c	6	2824.4	93.7	5742	14	ADZ64587	Adz64587 Expressio
c	7	2817.6	93.5	7940	14	ADZ64589	Adz64589 Expressio
c	8	2817.6	93.5	10769	14	ADZ64586	Adz64586 Expressio
c	9	2782	92.3	7677	10	ACF36695	Acf36695 Plasmid v
c	10	2759	91.5	5108	4	AAC86259	Aac86259 Plasmid G
c	11	2759	91.5	5108	4	AAC86258	Aac86258 Plasmid G
c	12	2759	91.5	5108	6	ABK53269	Abk53269 Growth ho
c	13	2759	91.5	5108	6	ABK53270	Abk53270 Growth ho
c	14	2759	91.5	5111	4	AAC86262	Aac86262 CMV IE pr
c	15	2759	91.5	5111	6	ABK53273	Abk53273 Growth ho
c	16	2759	91.5	5185	4	AAC86254	Aac86254 pGHRH-4 c
c	17	2759	91.5	5185	6	ABK53265	Abk53265 Growth ho
c	18	2759	91.5	5188	4	AAC86266	Aac86266 Plasmid G
c	19	2759	91.5	5188	6	ABK53277	Abk53277 Growth ho
c	20	2759	91.5	5254	4	AAC86267	Aac86267 Plasmid p
c	21	2759	91.5	5254	6	ABK85601	Abk85601 Growth ho
c	22	2754.2	91.4	5899	8	ABS55905	Abs55905 DNA plasm
c	23	2754.2	91.4	7528	4	AAF30316	Aaf30316 Bicistron
c	24	2746.2	91.1	7521	4	AAF30315	Aaf30315 Bicistron
c	25	2742.2	91.0	5845	8	ABS55904	Abs55904 DNA plasm
c	26	2717	90.1	5898	2	AAV00677	Aav00677 DNA plasm
c	27	2703.2	89.7	5843	2	AAV00676	Aav00676 DNA plasm
c	28	2677.4	88.8	4710	15	AEE68486	Aee68486 Plasmid v
c	29	2677.4	88.8	5398	15	AEE68485	Aee68485 Plasmid v
c	30	2677.4	88.8	5913	15	AEE68487	Aee68487 Plasmid v
c	31	2677.4	88.8	7765	15	AEE68505	Aee68505 Plasmid v
c	32	2677.4	88.8	7765	15	AEE68504	Aee68504 Plasmid v
c	33	2666	88.5	5302	13	ADU49659	Adu49659 Nucleotid
c	34	2665.2	88.4	5418	15	AEF63448	Aef63448 Plasmid p
c	35	2665.2	88.4	5444	15	AEF63461	Aef63461 Plasmid p
c	36	2665.2	88.4	5646	15	AEF63446	Aef63446 Plasmid p
c	37	2665.2	88.4	6690	15	AEF63454	Aef63454 Plasmid p
c	38	2665.2	88.4	6705	15	AEF63458	Aef63458 Plasmid C
c	39	2665.2	88.4	6903	15	AEF63456	Aef63456 Plasmid p
c	40	2665.2	88.4	6978	6	AAD38657	Aad38657 CMVkan/R-
c	41	2665.2	88.4	6978	10	ABZ58706	Abz58706 DNA seque
c	42	2665.2	88.4	7099	4	AAH22814	Aah22814 DNA seque
c	43	2665.2	88.4	8366	4	AAH22810	Aah22810 DNA seque
c	44	2665.2	88.4	8366	10	ABZ58698	Abz58698 DNA seque
c	45	2665.2	88.4	8900	15	AEF63450	Aef63450 Plasmid p

# ALIGNMENTS

## RESULT 1

ADQ91505

ID ADQ91505 standard; DNA; 3014 BP.

XX

AC ADQ91505;

XX

DT 21-OCT-2004 (first entry)

XX

DE Plasmid DNA including kanamycin resistance gene.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 02:58:50 ; Search time 8536.63 Seconds  
(without alignments)  
19743.258 Million cell updates/sec

Title: US-10-757-343-3  
Perfect score: 3014  
Sequence: 1 ggcgggccgctctagactag.....ggatccgcggccgctctaga 3014

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_est3:\*  
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4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_htc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
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1	901	29.9	905	14	DE097456	DE097456 Oryzias 1	
2	896	29.7	899	14	DE257891	DE257891 Oryzias 1	
3	895	29.7	898	14	DE105125	DE105125 Oryzias 1	



	4	893	29.6	896	14	DE101807	DE101807 Oryzias 1
	5	893	29.6	896	14	DE104670	DE104670 Oryzias 1
	6	893	29.6	896	14	DE255620	DE255620 Oryzias 1
c	7	892	29.6	893	14	DE101806	DE101806 Oryzias 1
c	8	890.2	29.5	951	8	CV983341	CV983341 UMC-bof_0
	9	890	29.5	893	14	DE104917	DE104917 Oryzias 1
	10	889	29.5	892	14	DE104869	DE104869 Oryzias 1
c	11	886.4	29.4	894	9	DN641029	DN641029 UMC-bend_
	12	885	29.4	888	14	DE097133	DE097133 Oryzias 1
	13	883	29.3	886	14	DE102263	DE102263 Oryzias 1
c	14	882	29.3	883	14	DE097316	DE097316 Oryzias 1
c	15	882	29.3	883	14	DE264014	DE264014 Oryzias 1
	16	882	29.3	885	14	DE258042	DE258042 Oryzias 1
	17	881	29.2	884	14	DE096890	DE096890 Oryzias 1
c	18	877.4	29.1	1048	8	CO552396	CO552396 AcLy4_50
	19	877	29.1	880	14	DE256544	DE256544 Oryzias 1
c	20	876	29.1	876	14	DE098337	DE098337 Oryzias 1
c	21	874	29.0	875	14	DE104916	DE104916 Oryzias 1
c	22	873	29.0	873	14	DE257460	DE257460 Oryzias 1
	23	873	29.0	876	14	DE097980	DE097980 Oryzias 1
	24	872	28.9	875	14	DE097115	DE097115 Oryzias 1
	25	872	28.9	875	14	DE097211	DE097211 Oryzias 1
	26	870	28.9	873	14	DE104479	DE104479 Oryzias 1
	27	870	28.9	873	14	DE265629	DE265629 Oryzias 1
	28	868.4	28.8	873	14	DE098619	DE098619 Oryzias 1
	29	868	28.8	871	14	DE097113	DE097113 Oryzias 1
	30	868	28.8	871	14	DE097317	DE097317 Oryzias 1
	31	868	28.8	871	14	DE097534	DE097534 Oryzias 1
	32	868	28.8	871	14	DE098058	DE098058 Oryzias 1
	33	868	28.8	871	14	DE255532	DE255532 Oryzias 1
	34	868	28.8	871	14	DE257461	DE257461 Oryzias 1
	35	868	28.8	871	14	DE264015	DE264015 Oryzias 1
	36	866.4	28.7	871	14	DE096695	DE096695 Oryzias 1
	37	864.8	28.7	879	14	DE098022	DE098022 Oryzias 1
c	38	864	28.7	865	14	DE261593	DE261593 Oryzias 1
	39	864	28.7	867	14	DE097420	DE097420 Oryzias 1
	40	863	28.6	866	14	DE097434	DE097434 Oryzias 1
	41	863	28.6	866	14	DE098498	DE098498 Oryzias 1
	42	863	28.6	866	14	DE103082	DE103082 Oryzias 1
	43	863	28.6	866	14	DE104168	DE104168 Oryzias 1
	44	863	28.6	866	14	DE104911	DE104911 Oryzias 1
	45	863	28.6	866	14	DE256736	DE256736 Oryzias 1

# ALIGNMENTS

## RESULT 1

DE097456

LOCUS DE097456 905 bp DNA linear GSS 15-SEP-2005  
DEFINITION Oryzias latipes DNA, clone: ola1-127I23.R, genomic survey sequence.  
ACCESSION DE097456  
VERSION DE097456.1 GI:68151055  
KEYWORDS GSS.  
SOURCE Oryzias latipes (Japanese medaka)  
ORGANISM Oryzias latipes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;